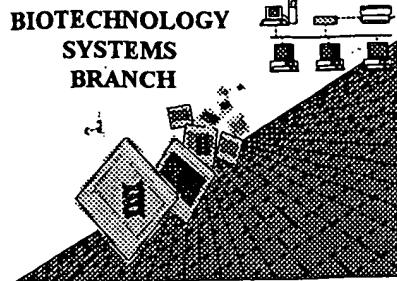


4570  
0815



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/758,017

Source: 01PE

Date Processed by STIC: 8/17/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

**Raw Sequence Listing Error Summary**

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER: 09/758,017</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 3 <sup>rd</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/758,017

DATE: 08/17/2001  
TIME: 12:01:30

Input Set : A:\U0132093.app  
Output Set: N:\CRF3\08162001\1758017.raw

ppn 1-2

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Lanes, Olav  
4 Willasen, Nils Peder  
5 Guddal, Per Henrik  
6 Gjellesvik, Dag Rune  
8 <120> TITLE OF INVENTION: Cod uracil-DNA glycosylase, gene coding therefore,  
9 recombinant DNA containing said gene or operative parts  
10 thereof, a method for preparing said protein and the  
11 use of said protein or said operative pa  
13 <130> FILE REFERENCE: U013209-3  
15 <140> CURRENT APPLICATION NUMBER: 09/758,017  
16 <141> CURRENT FILING DATE: 2001-01-10  
18 <150> PRIOR APPLICATION NUMBER: 2000 5428  
19 <151> PRIOR FILING DATE: 2000-10-27  
21 <150> PRIOR APPLICATION NUMBER: 2000 0163  
22 <151> PRIOR FILING DATE: 2000-01-12  
24 <160> NUMBER OF SEQ ID NOS: 19  
26 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

```

131 <210> SEQ ID NO: 2
132 <211> LENGTH: 301
133 <212> TYPE: PRT
134 <213> ORGANISM: Gadus morhua
136 <400> SEQUENCE: 2
137 Met Leu Phe Lys Leu Gly Leu Cys Gln Arg Cys Ile Ser Ser Asn Arg
138 1 5 10 15
E--> 140 Xaa Leu Pro Gly Leu Leu Ile Pro Gln Thr Leu Cys Phe Ser Lys Leu
141 20 25 30
143 Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser Asn Val Glu Gln Lys
144 35 40 45
146 Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu Glu Arg Met Ala Lys
147 50 55 60
149 Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala Lys Ala Thr Pro Ala
150 65 70 75 80
152 Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala Ala Glu Phe Glu Lys
153 85 90 95
155 Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala Asp Glu Arg Ser Arg
156 100 105 110
158 His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr Ser Ser Thr Glu Met
159 115 120 125
161 Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu Gly Gln Asp Pro Tyr
162 130 135 140
164 His Gly Pro Asn Gln Ala His Gly Leu Cys Phe Ser Val Gln Lys Pro
165 145 150 155 160
167 Val Pro Pro Pro Ser Leu Val Asn Ile Tyr Lys Glu Leu Cys Thr

```

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/758,017

DATE: 08/17/2001  
TIME: 12:01:31

Input Set : A:\U0132093.app  
Output Set: N:\CRF3\08162001\I758017.raw

168	165	170	175
170	Asp Ile Asp Gly Phe Lys His Pro Gly His Gly Asp Leu Ser Gly Trp		
171	180	185	190
173	Ala Lys Gln Gly Val Leu Leu Leu Asn Ala Val Leu Thr Val Arg Ala		
174	195	200	205
176	His Gln Ala Asn Ser His Lys Asp Arg Gly Trp Glu Thr Phe Thr Asp		
177	210	215	220
179	Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu Gly Val Val Phe Leu		
180	225	230	235
182	240		
183	Leu Trp Gly Ser Tyr Ala His Lys Lys Gly Ala Thr Ile Asp Arg Lys		
185	245	250	255
186	Arg His His Val Leu Gln Ala Val His Pro Ser Pro Leu Ser Ala His		
188	260	265	270
189	Arg Gly Phe Leu Gly Cys Lys His Phe Ser Lys Ala Asn Gly Leu Leu		
191	275	280	285
192	Lys Leu Ser Gly Thr Glu Pro Ile Asn Trp Arg Ala Leu		
	290	295	300

*PSJ*  
Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/758,017

DATE: 08/17/2001  
TIME: 12:01:32

Input Set : A:\U0132093.app  
Output Set: N:\CRF3\08162001\I758017.raw

L:43 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:43 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:140 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2